

SEQUENCE LISTING

<110> National Institute of Advanced Industrial Science and Technology

<120> Lethal gene markers for transformant selection

<130> -23603055

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<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 1

gctgatgctg cattgagttc tgctatgg

28

<210> 2

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 2

gtttaatcca atttaagtcc cataacttgg ccgctatggc ctc当地 57

<210> 3

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 3

caagaaatat ctttgaggcc atagcggcca agttatggga ct当地 57

<210> 4

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 4

tcatccctga taatatttga tcaccaat

28

<210> 5

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 5

gcatggccgc ctcggccgaa aggtttaaa gattacgggc atg

43

<210> 6

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 6

cgatgaattc tcaccaatca ccatcacgat aatc

34

<210> 7

<211> 598

<212> DNA

<213> E.coli

<400> 7

gcatggccgc ctcggccgaa aggtttaaa gattacgggc atgattatca tccagctccg 60  
aaaactgaga atattaaagg gcttggtgat cttaagcctg ggataccaaa aacaccaaag 120  
cagaatggtg gtggaaaacg caagcgctgg actggagata aagggcgtaa gatttatgag 180  
tgggattctc agcatggtga gcttgagggg tatcgtgcc a gtatggtca gcatcttggc 240  
tcatttgacc ctaaaacagg caatcagttg aaaggtccag atccgaaacg aaatatcaag 300  
aaatatctt gaggccatag cggccaagtt atggactta aattggattt aacttggttt 360  
gataaaaagta cagaagattt taagggtgag gagtattcaa aagattttgg agatgacggt 420  
tcagttatgg aaagtctagg tgtgccttt aaggataatg ttaataacgg ttgccttgat 480  
gttatacgctg aatgggtacc tttgctacaa ccataactta atcatcaa at tcatattcc 540  
gataatgagt atttgtttc gtttgattat cgtgatggtg attggtgaga attcatcg 598

<210> 8

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 8

tagtagtagt agtagaaagg ttttaaagat tacgggcattg

40

<210> 9

<211> 46

<212> DNA

<213> E.coli

<400> 9

gcatggccgc ctcggccgta gaaagggtttt aaagattacg ggcattg

46

<210> 10

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

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<210> 11

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 11

gcatggccgc ctcggccgta gtagtagaaa ggttttaag attacggca tg

52

<210> 12

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 12

gcatggccgc ctcggccgta gtagtagtag aaaggttta aagattacgg gcatg

55

<210> 13

<211> 58

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 13

gcatggccgc ctcggccgta gtagtagtag tagaaagggtt ttaaagatta cgggcattg 58

<210> 14

<211> 607

<212> DNA

<213> E.coli

<400> 14

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acacccaaagc agaatggtgg tggaaaacgc aagcgctgga ctggagataa agggcgtaag 180  
atttatgagt gggattctca gcatggtgag cttgaggggt atcgtgccag tgatggtcag 240  
catcttggct catttgaccc taaaacaggc aatcagttga aaggtccaga tccgaaacga 300  
aatatcaaga aatatcttg agccatagc ggccaagttt tggacttaa attggattta 360  
acttggtttg ataaaagtac agaagatttt aagggtgagg agtattcaaa agattttgg 420  
gatgacggtt cagttatgga aagtcttaggt gtgcctttta aggataatgt taataacggt 480  
tgctttgatg ttatagctga atgggtacct ttgctacaac catacttaa tcatcaaatt 540

gatatttccg ataatgagta tttgtttcg tttgattatc gtgatggta ttggtagaa 600  
ttcatcg 607

<210> 15

<211> 258

<212> DNA

<213> E.coli

<400> 15

atggactta aattggattt aactggttt gataaaagta cagaagattt taagggtgag 60  
gagtattcaa aagattttgg agatgacggt tcagttatgg aaagtctagg tgtgccttt 120  
aaggataatg ttaataacgg ttgccttgat gttatagctg aatgggtacc ttgcataaa 180  
ccatacttta atcatcaa at tgatattcc gataatgagt atttgttcc gtttgattat 240  
cgtgatggtg attggta 258

<210> 16

<211> 3066

<212> DNA

<213> E.coli

<400> 16

aactcggtt taatcagacc tggcatgagt ggaagcggga cgaacagcac aggcaacaac 60  
aacgcccggcc cgggcacttc cggggcatga gtatgtgata tccggggctg caccccgac 120  
cccgccaaaca catcacgggc cacaaaattt tttgtggccc gctctgcgtt ttctaaatgt 180  
tatccctcct gatttctaaa aaatttcca cctgaacttg acagaaaaaa cgatgacgag 240

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gcattatcgg cagctattgc tgatattatg gctgccctga aaggaccgtt taaatttgg 720  
ctttgggggg tggctttata tggtagtttgc ccatcacaaa tagcgaaaga tgaccccaat 780  
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tctcagcatg gtgagcttga gggtatcgt gccagtatcgt gtcagcatct tggctcattt 1920  
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cgatcg 3066

<210> 17

<211> 551

<212> PRT

<213> E.coli

<400> 17

Met Ser Gly Gly Asp Gly Arg Gly His Asn Thr Gly Ala His Ser Thr  
1 5 10 15

Ser Gly Asn Ile Asn Gly Gly Pro Thr Gly Leu Gly Val Gly Gly  
20 25 30

Ala Ser Asp Gly Ser Gly Trp Ser Ser Glu Asn Asn Pro Trp Gly Gly  
35 40 45

Gly Ser Gly Ser Gly Ile His Trp Gly Gly Ser Gly His Gly Asn  
50 55 60

Gly Gly Gly Asn Gly Asn Ser Gly Gly Ser Gly Thr Gly Gly Asn  
65 70 75 80

Leu Ser Ala Val Ala Ala Pro Val Ala Phe Gly Phe Pro Ala Leu Ser  
85 90 95

Thr Pro Gly Ala Gly Gly Leu Ala Val Ser Ile Ser Ala Gly Ala Leu  
100 105 110

Ser Ala Ala Ile Ala Asp Ile Met Ala Ala Leu Lys Gly Pro Phe Lys  
115 120 125

Phe Gly Leu Trp Gly Val Ala Leu Tyr Gly Val Leu Pro Ser Gln Ile

130 135 140  
Ala Lys Asp Asp Pro Asn Met Met Ser Lys Ile Val Thr Ser Leu Pro  
145 150 155 160  
Ala Asp Asp Ile Thr Glu Ser Pro Val Ser Ser Leu Pro Leu Asp Lys  
165 170 175  
Ala Thr Val Asn Val Asn Val Arg Val Val Asp Asp Val Lys Asp Glu  
180 185 190  
Arg Gln Asn Ile Ser Val Val Ser Gly Val Pro Met Ser Val Pro Val  
195 200 205  
Val Asp Ala Lys Pro Thr Glu Arg Pro Gly Val Phe Thr Ala Ser Ile  
210 215 220  
Pro Gly Ala Pro Val Leu Asn Ile Ser Val Asn Asn Ser Thr Pro Ala  
225 230 235 240  
Val Gln Thr Leu Ser Pro Gly Val Thr Asn Asn Thr Asp Lys Asp Val  
245 250 255  
Arg Pro Ala Gly Phe Thr Gln Gly Gly Asn Thr Arg Asp Ala Val Ile  
260 265 270  
Arg Phe Pro Lys Asp Ser Gly His Asn Ala Val Tyr Val Ser Val Ser

275

280

285

Asp Val Leu Ser Pro Asp Gln Val Lys Gln Arg Gln Asp Glu Glu Asn  
290 295 300

Arg Arg Gln Gln Glu Trp Asp Ala Thr His Pro Val Glu Ala Ala Glu  
305 310 315 320

Arg Asn Tyr Glu Arg Ala Arg Ala Glu Leu Asn Gln Ala Asn Glu Asp  
325 330 335

Val Ala Arg Asn Gln Glu Arg Gln Ala Lys Ala Val Gln Val Tyr Asn  
340 345 350

Ser Arg Lys Ser Glu Leu Asp Ala Ala Asn Lys Thr Leu Ala Asp Ala  
355 360 365

Ile Ala Glu Ile Lys Gln Phe Asn Arg Phe Ala His Asp Pro Met Ala  
370 375 380

Gly Gly His Arg Met Trp Gln Met Ala Gly Leu Lys Ala Gln Arg Ala  
385 390 395 400

Gln Thr Asp Val Asn Asn Lys Gln Ala Ala Phe Asp Ala Ala Ala Lys  
405 410 415

Glu Lys Ser Asp Ala Asp Ala Ala Leu Ser Ser Ala Met Glu Ser Arg

420 425 430

Lys Lys Lys Glu Asp Lys Lys Arg Ser Ala Glu Asn Asn Leu Asn Asp  
435 440 445

Glu Lys Asn Lys Pro Arg Lys Gly Phe Lys Asp Tyr Gly His Asp Tyr  
450 455 460

His Pro Ala Pro Lys Thr Glu Asn Ile Lys Gly Leu Gly Asp Leu Lys  
465 470 475 480

Pro Gly Ile Pro Lys Thr Pro Lys Gln Asn Gly Gly Gly Lys Arg Lys  
485 490 495

Arg Trp Thr Gly Asp Lys Gly Arg Lys Ile Tyr Glu Trp Asp Ser Gln  
500 505 510

His Gly Glu Leu Glu Gly Tyr Arg Ala Ser Asp Gly Gln His Leu Gly  
515 520 525

Ser Phe Asp Pro Lys Thr Gly Asn Gln Leu Lys Gly Pro Asp Pro Lys  
530 535 540

Arg Asn Ile Lys Lys Tyr Leu  
545 550

<210> 18

<211> 110

<212> PRT

<213> E.coli

<400> 18

Ala Glu Asn Asn Leu Asn Asp Glu Lys Asn Lys Pro Arg Lys Gly Phe  
1 5 10 15

Lys Asp Tyr Gly His Asp Tyr His Pro Ala Pro Lys Thr Glu Asn Ile  
20 25 30

Lys Gly Leu Gly Asp Leu Lys Pro Gly Ile Pro Lys Thr Pro Lys Gln  
35 40 45

Asn Gly Gly Gly Lys Arg Lys Arg Trp Thr Gly Asp Lys Gly Arg Lys  
50 55 60

Ile Tyr Glu Trp Asp Ser Gln His Gly Glu Leu Glu Gly Tyr Arg Ala  
65 70 75 80

Ser Asp Gly Gln His Leu Gly Ser Phe Asp Pro Lys Thr Gly Asn Gln  
85 90 95

Leu Lys Gly Pro Asp Pro Lys Arg Asn Ile Lys Lys Tyr Leu  
100 105 110

<210> 19

<211> 97

<212> PRT

<213> E.coli

<400> 19

Lys Gly Phe Lys Asp Tyr Gly His Asp Tyr His Pro Ala Pro Lys Thr  
1 5 10 15.

Glu Asn Ile Lys Gly Leu Gly Asp Leu Lys Pro Gly Ile Pro Lys Thr  
20 25 30

Pro Lys Gln Asn Gly Gly Lys Arg Lys Arg Trp Thr Gly Asp Lys  
35 40 45

Gly Arg Lys Ile Tyr Glu Trp Asp Ser Gln His Gly Glu Leu Glu Gly  
50 55 60

Tyr Arg Ala Ser Asp Gly Gln His Leu Gly Ser Phe Asp Pro Lys Thr  
65 70 75 80

Gly Asn Gln Leu Lys Gly Pro Asp Pro Lys Arg Asn Ile Lys Lys Tyr  
85 90 95

Leu

<210> 20

<211> 330

<212> DNA

<213> E.coli

<400> 1

ggccgcctcg gccgtagtag tagaaagggtt ttaaagatta cgggcatgtatcatccag 60  
ctccgaaaac tgagaatatt aaaggccttg gtgatcttaa gcctggata ccaaaaacac 120  
caaagcagaa tgggtggaa aaacgcaagc gctggactgg agataaaggg cgtaagattt 180  
atgagtggaa ttctcagcat ggtgagcttg aggggtatcg tgccagtgtat ggtcagcatc 240  
ttggctcatt tgaccctaaa acaggcaatc agttgaaagg tccagatccg aaacgaaata 300  
tcaagaaata tcttgaggc catagcggcc 330

<210> 21

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:adapter

<400> 2

gatccccggg taccgaggcc gcctcgcccg agctcgaatt cggccggcca tagcggccgc 60

<210> 22

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:adapter

<400> 3

aattgcggcc gctatggccg gccgaattcg agctcggccg aggccgcctc ggtacccggg 60

<210> 23

<211> 650

<212> DNA

<213> S.cerevisiae

<400> 4

ggccgcctcg gccaggatct ggtggcgaac aagcatgcga tatttgcga cttaaaaagc 60  
tcaagtgctc caaagaaaaa ccgaagtgcg ccaagtgtct gaagaacaac tggagtg 120  
gctactctcc caaaacccaa aggtctccgc tgacttaggc acatctgaca gaagtgg 180  
caaggctaga aagactggaa cagctatttc tactgatttt tcctcgagaa gaccttgaca 240  
tgattttgaa aatggattct ttacaggata taaaagcatt gttAACAGGA ttatttg 300  
aagataatgt gaataaagat gccgtcacag atagattggc ttcaGTggag actgatatgc 360  
ctctaacatt gagacagcat agaataagtg cgacatcatc atcggaaagag agtagtaaca 420  
aaggtaaaag acagttgact gtatcgattt actcggcagc tcatcatgat aactccacaa 480

ttcgttgga tttatgccc agggatgctc ttcatggatt tgattggct gaagaggatg 540  
acatgtcgga tggcttgcctt ttcctgaaaa cggacccaa caataatggg ttctttggcg 600  
acggttctctt ctatgttattt cttcgctgac tgactgaggc catagcggcc 650

<210> 24

<211> 535

<212> DNA

<213> A. oryzae

<400> 5

ggccgcctcg gccattacta gtctactagt aactctgtct tatcgtcatc tccatagg 60  
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ttttgttac ggttagccatg acccctccat ggcaaagaga gaggaggacg aggacgatca 180  
ggaaactgtg tctcgccgtc ataccacaat cgttttatcc tgattgacat cttcttaat 240  
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